



1200029-US2.ST25.txt
SEQUENCE LISTING

<110> Soll, Dieter
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<140> 10/661,399
<141> 2003-09-12
<150> 60/037,275
<151> 1997-02-03
<150> PCT/US98/01860
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<213> Bacillus subtilis

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His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu
35          40          45

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Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln
50 55 60

Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr
65 70 75 80

Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met
85 90 95

Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys
100 105 110

Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu
115 120 125

Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu
130 135 140

Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val
145 150 155 160

Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala
165 170 175

Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu
180 185 190

Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met
195 200 205

Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr
210 215 220

Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr
225 230 235 240

Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu
245 250 255

Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr
260 265 270

Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser
275 280 285

Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser

290

295

Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys
305 310 315 320

Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly
325 330 335

Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg
340 345 350

Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp
355 360 365

Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser
370 375 380

Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu
385 390 395 400

Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala
405 410 415

Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser
420 425 430

Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser
435 440 445

Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly
450 455 460

Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr
465 470 475 480

Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly
485 490 495

Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala
500 505 510

Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu
515 520 525

Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys
530 535 540

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Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile
545 550 555 560

Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met
565 570 575

Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His
580 585 590

Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gln
595 600 605

Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn
610 615 620

Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys
625 630 635 640

Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn
645 650 655

Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val
660 665 670

Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu
675 680 685

Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe
690 695 700

Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro
705 710 715 720

Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys
725 730 735

Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu
740 745 750

Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg Gln Gly
755 760 765

Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr Pro Glu
770 775 780

Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr
785 790 795 800

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Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala
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Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr
820 825 830

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835 840 845

His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe Phe Ile
850 855 860

Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu
865 870 875 880

Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro
885 890 895

Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys
900 905 910

Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Glu
915 920 925

Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys
930 935 940

Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala
945 950 955 960

Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn
965 970 975

Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu
980 985 990

Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser Lys Ile
995 1000 1005

Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp Ala
1010 1015 1020

Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
1025 1030 1035

Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro
1040 1045 1050

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Gln Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly
 1055 1060 1065

Phe Leu Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn
 1070 1075 1080

Pro Pro Met Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
 1085 1090 1095

Lys Ser Ser Pro Arg Leu Leu Phe Leu Trp Ser Asn Asp Lys Asp
 1100 1105 1110

Lys Met Arg Ala Arg Ser Leu Ser Thr Ser Leu Ser Leu Val Pro
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Ala Lys Leu Asp Ser Met Pro Leu Ser Ala Cys Ala Val Tyr Pro
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Glu Ser Ile Leu Pro Arg Asp Lys His Gly Asp Ile
 1145 1150 1155

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 <213> Bacillus subtilis

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aaa aaa gag att aag att tct gat ctg gtt gat gaa tct tat aaa cgc 96
 Lys Lys Glu Ile Lys Ile Ser Asp Leu Val Asp Glu Ser Tyr Lys Arg
 20 25 30

atc caa gcg gtt gat gat aag gta caa gcc ttt ttg gca tta gat gaa 144
 Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu
 35 40 45

gaa aga gcg cgc gca tac gcg aag gag ctt gat gag gcg gtt gac ggc 192
 Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly
 50 55 60

cgt tct gag cac ggt ctt ctt ttc ggt atg ccg atc ggc gta aaa gat 240
 Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp
 65 70 75 80

aat atc gta aca aaa ggg ctg cgc aca aca tgc tcc agc aaa att ctc 288

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Glu	Asn	Phe	Asp	Pro	Ile	Tyr	Asp	Ala	Thr	Val	Val	Gln	Arg	Leu	Gln		
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Asp	Ala	Glu	Ala	Val	Thr	Ile	Gly	Lys	Leu	Asn	Met	Asp	Glu	Phe	Ala		
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atg	ggg	tca	tct	aca	gaa	aac	tca	gct	tac	aag	ctg	acg	aaa	aac	cct	432	
Met	Gly	Ser	Ser	Thr	Glu	Asn	Ser	Ala	Tyr	Lys	Leu	Thr	Lys	Asn	Pro		
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tgg	aac	ctg	gat	aca	gtt	ccc	ggc	ggg	tca	agc	ggc	gga	tct	gca	gct	480	
Trp	Asn	Leu	Asp	Thr	Val	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	Ala		
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340 345 350	
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Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser	
355 360 365	
ggc tac tac gat gcg tac tac aaa aaa gcg caa aaa gtg cgt acg ttg	1152
Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu	
370 375 380	
att aag aag gat ttc gag gac gta ttt gaa aaa tat gat gtt att gtt	1200
Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val	
385 390 395 400	
gga ccg act aca ccg aca cct gcg ttt aaa atc ggt gaa aac acg aag	1248
Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys	
405 410 415	
gat ccg ctc aca atg tac gca aac gat atc tta acg att ccg gtc aac	1296
Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn	
420 425 430	
ctt gcg gcg tac cgg gaa tca ggt gcc atg cgg tta gca gac gga ctt	1344
Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu	
435 440 445	
ccg ctc ggc ctg caa atc atc gga aaa cac ttt gat gaa gca ctg tat	1392
Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr	
450 455 460	
acc gcg ttg ctc atg cat ttg aac aag caa gag acc atc ata aag caa	1440
Thr Ala Leu Leu Met His Leu Asn Lys Gln Glu Thr Ile Ile Lys Gln	
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aac ctg aac tgt aag ggg tga	1461
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20 25 30
Ile Gln Ala Val Asp Asp Lys Val Gln Ala Phe Leu Ala Leu Asp Glu
35 40 45
Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu Asp Glu Ala Val Asp Gly
50 55 60

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Arg Ser Glu His Gly Leu Leu Phe Gly Met Pro Ile Gly Val Lys Asp
 65 70 75 80
 Asn Ile Val Thr Lys Gly Leu Arg Thr Thr Cys Ser Ser Lys Ile Leu
 85 90 95
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 100 105 110
 Asp Ala Glu Ala Val Thr Ile Gly Lys Leu Asn Met Asp Glu Phe Ala
 115 120 125
 Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr Lys Leu Thr Lys Asn Pro
 130 135 140
 Trp Asn Leu Asp Thr Val Pro Gly Gly Ser Ser Gly Gly Ser Ala Ala
 145 150 155 160
 Ala Val Ala Ala Gly Glu Val Pro Phe Ser Leu Gly Ser Asp Thr Gly
 165 170 175
 Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys Gly Val Val Gly Leu Lys
 180 185 190
 Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly Leu Val Ala Phe Ala Ser
 195 200 205
 Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg Thr Val Glu Asp Asn Ala
 210 215 220
 Phe Leu Leu Gln Ala Ile Ser Gly Val Asp Lys Met Asp Ser Thr Ser
 225 230 235 240
 Ala Asn Val Asp Val Pro Asp Phe Leu Ser Ser Leu Thr Gly Asp Ile
 245 250 255
 Lys Gly Leu Lys Ile Ala Val Pro Lys Glu Tyr Leu Gly Glu Gly Val
 260 265 270
 Gly Lys Glu Ala Arg Glu Ser Val Leu Ala Ala Leu Lys Val Leu Glu
 275 280 285
 Gly Leu Gly Ala Thr Trp Glu Glu Val Ser Leu Pro His Ser Lys Tyr
 290 295 300
 Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser Ser Glu Ala Ser Ala Asn
 305 310 315 320

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Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly Tyr Arg Thr Asp Asn Ala
325 330 335

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340 345 350

Asn Glu Val Lys Arg Arg Ile Met Leu Gly Thr Phe Ala Leu Ser Ser
355 360 365

Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala Gln Lys Val Arg Thr Leu
370 375 380

Ile Lys Lys Asp Phe Glu Asp Val Phe Glu Lys Tyr Asp Val Ile Val
385 390 395 400

Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys Ile Gly Glu Asn Thr Lys
405 410 415

Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile Leu Thr Ile Pro Val Asn
420 425 430

Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met Arg Leu Ala Asp Gly Leu
435 440 445

Pro Leu Gly Leu Gln Ile Ile Gly Lys His Phe Asp Glu Ala Leu Tyr
450 455 460

Thr Ala Leu Leu Met His Leu Asn Lys Gln Glu Thr Ile Ile Lys Gln
465 470 475 480

Asn Leu Asn Cys Lys Gly
485

<210> 5
<211> 1431
<212> DNA
<213> Bacillus subtilis

<220>
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<222> (1)..(1428)
<223> subunit B, corresponds to nucleotides 1876 - 3306 of SEQ ID NO: 1

<220>
<221> misc_feature
<222> (152)..(152)
<223> Xaa is Phe, Ser, Tyr, or Cys

<220>
<221> misc_feature

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<222> (164)..(164)

<223> Xaa is Ser, Pro, Thr, or Ala

<220>

<221> misc_feature

<222> (455)..(490)

<223> n is a, c, t, or g

<400> 5

ttg	aac	ttt	gaa	acg	gta	atc	gga	ctt	gaa	gtc	cac	ggt	gag	tta	aaa	48
Leu	Asn	Phe	Glu	Thr	Val	Ile	Gly	Leu	Glu	Val	His	Val	Glu	Leu	Lys	
1				5				10					15			

aca	aaa	tca	aaa	att	ttc	tca	agc	tct	cca	acg	cca	ttc	ggc	gcg	gag	96
Thr	Lys	Ser	Lys	Ile	Phe	Ser	Ser	Ser	Pro	Thr	Pro	Phe	Gly	Ala	Glu	
			20					25					30			

gcg	aat	acg	cag	aca	agc	gtt	att	gac	ctc	gga	tat	ccg	ggc	gtc	ctg	144
Ala	Asn	Thr	Gln	Thr	Ser	Val	Ile	Asp	Leu	Gly	Tyr	Pro	Gly	Val	Leu	
		35					40					45				

cct	gtt	ctg	aac	aaa	gaa	gcc	gtt	gaa	ttc	gca	atg	aaa	gcc	gct	atg	192
Pro	Val	Leu	Asn	Lys	Glu	Ala	Val	Glu	Phe	Ala	Met	Lys	Ala	Ala	Met	
	50					55					60					

gcg	ctc	aac	tgt	gag	atc	gca	acg	gat	acg	aag	ttt	gac	cgc	aaa	aac	240
Ala	Leu	Asn	Cys	Glu	Ile	Ala	Thr	Asp	Thr	Lys	Phe	Asp	Arg	Lys	Asn	
65				70					75					80		

tat	ttc	tat	cct	gac	aac	ccg	aaa	gcg	tat	cag	att	tct	caa	ttt	gat	288
Tyr	Phe	Tyr	Pro	Asp	Asn	Pro	Lys	Ala	Tyr	Gln	Ile	Ser	Gln	Phe	Asp	
				85				90						95		

aag	cca	atc	ggc	gaa	aac	ggc	tgg	atc	gaa	att	gaa	gtc	ggc	ggc	aaa	336
Lys	Pro	Ile	Gly	Glu	Asn	Gly	Trp	Ile	Glu	Ile	Glu	Val	Gly	Gly	Lys	
			100					105					110			

aca	aaa	cgc	atc	ggc	atc	acg	cgc	ctt	cat	ctt	gaa	gag	gat	gcc	gga	384
Thr	Lys	Arg	Ile	Gly	Ile	Thr	Arg	Leu	His	Leu	Glu	Glu	Asp	Ala	Gly	
		115					120					125				

aaa	ctg	acg	cat	acg	ggc	gac	ggc	tat	tct	ctt	gtt	gac	ttc	aac	cgt	432
Lys	Leu	Thr	His	Thr	Gly	Asp	Gly	Tyr	Ser	Leu	Val	Asp	Phe	Asn	Arg	
	130					135					140					

caa	gga	acg	ccg	ctt	gtt	gag	tnc	gta	tca	gag	ccg	gac	atc	cgc	acg	480
Gln	Gly	Thr	Pro	Leu	Val	Glu	Xaa	Val	Ser	Glu	Pro	Asp	Ile	Arg	Thr	
145				150						155					160	

ccg	gaa	gaa	ncg	tac	gca	tat	ctt	gaa	aag	ctg	aaa	tcc	atc	atc	caa	528
Pro	Glu	Glu	Xaa	Tyr	Ala	Tyr	Leu	Glu	Lys	Leu	Lys	Ser	Ile	Ile	Gln	
				165				170						175		

tat	aca	ggc	gtt	tct	gac	tgt	aaa	atg	gaa	gaa	ggc	tca	ctt	cgc	tgt	576
Tyr	Thr	Gly	Val	Ser	Asp	Cys	Lys	Met	Glu	Glu	Gly	Ser	Leu	Arg	Cys	
			180					185					190			

gac	gcc	aat	atc	tct	ctt	cgt	ccg	atc	ggc	caa	gag	gaa	ttc	ggc	aca	624
Asp	Ala	Asn	Ile	Ser	Leu	Arg	Pro	Ile	Gly	Gln	Glu	Glu	Phe	Gly	Thr	
		195					200					205				

aaa	aca	gaa	ttg	aaa	aac	ttg	aac	tcc	ttt	gcg	ttt	gtt	caa	aaa	ggc	672
Lys	Thr	Glu	Leu	Lys	Asn	Leu	Asn	Ser	Phe	Ala	Phe	Val	Gln	Lys	Gly	

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210	215	220	
ctt gag cat gaa gaa aaa cgc cag gag cag gtt ctt ctt tcc ggc ttc Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe 225 230 235 240			720
ttc atc cag caa gaa act cgc cgt tat gat gaa gca acg aag aaa acc Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr 245 250 255			768
att ctt atg cgt gtc aaa gag gga tct gac gac tac cgt tac ttt cca Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro 260 265 270			816
gag cca gat cta gtc gag ctc tac att gat gat gaa tgg aag gaa cgc Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg 275 280 285			864
gta aaa gca agc att cct gag ctt ccg gat gag cgc cgc aag cgt tat Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr 290 295 300			912
atc gaa gag ctt ggc ttc gct gca tat gac gca atg gtt ctg acg ctg Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu 305 310 315 320			960
aca aaa gaa atg gct gat ttc ttc gaa gaa acc gtt caa aaa ggc gct Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala 325 330 335			1008
gaa gct aaa caa gcg tct aac tgg ctg atg ggt gaa gtg tca gct tac Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr 340 345 350			1056
cta aac gca gaa caa aaa gag ctt gcc gat gtt gcc ctg aca cct gaa Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu 355 360 365			1104
ggc ctt gcc ggc atg atc aaa ttg att gaa aaa gga acc att tct tct Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser 370 375 380			1152
aag atc gcg aag aaa gtg ttt aaa gaa ttg att gaa aaa ggc ggc gac Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp 385 390 395 400			1200
gct gag aag att gtg aaa gag aaa ggc ctt gtt cag att tct gac gaa Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu 405 410 415			1248
ggc gtg ctt ctg aag ctt gtc act gag gcg ctt gac aac aat cct caa Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln 420 425 430			1296
tca atc gaa gac ttt aaa aac gga aaa gac gcg atc ggc ttc cta Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu 435 440 445			1344
gtc gga cag att atg aaa gcg tcc aaa gga caa gcc aac ccg ccg atg Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met 450 455 460			1392
gtc aac aaa att ctg ctt gaa gaa att aaa aaa cgc taa			1431

Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
 465 470 475

<210> 6
 <211> 476
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> MISC_FEATURE
 <222> (152)..(152)
 <223> Xaa is Phe, Ser, Tyr, or Cys

<220>
 <221> MISC_FEATURE
 <222> (164)..(164)
 <223> Xaa is Ser, Pro, Thr, or Ala

<400> 6

Leu Asn Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys
 1 5 10 15

Thr Lys Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu
 20 25 30

Ala Asn Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu
 35 40 45

Pro Val Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met
 50 55 60

Ala Leu Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn
 65 70 75 80

Tyr Phe Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp
 85 90 95

Lys Pro Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys
 100 105 110

Thr Lys Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly
 115 120 125

Lys Leu Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg
 130 135 140

Gln Gly Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr
 145 150 155 160

Pro Glu Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln
 165 170 175

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Tyr Thr Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys
 180 185 190
 Asp Ala Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr
 195 200 205
 Lys Thr Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly
 210 215 220
 Leu Glu His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe
 225 230 235 240
 Phe Ile Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr
 245 250 255
 Ile Leu Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro
 260 265 270
 Glu Pro Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg
 275 280 285
 Val Lys Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr
 290 295 300
 Ile Glu Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu
 305 310 315 320
 Thr Lys Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala
 325 330 335
 Glu Ala Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr
 340 345 350
 Leu Asn Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu
 355 360 365
 Gly Leu Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser
 370 375 380
 Lys Ile Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp
 385 390 395 400
 Ala Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
 405 410 415
 Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro Gln

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420

425

430

Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly Phe Leu
 435 440 445

Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn Pro Pro Met
 450 455 460

Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
 465 470 475

<210> 7

<211> 291

<212> DNA

<213> Bacillus subtilis

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<221> CDS

<222> (1)..(288)

<223> Subunit C, corresponds to nucleotides 103 - 393 of SEQ ID NO: 1

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atg tca cga att tca ata gaa gaa gta aag cac gtt gcg cac ctt gca 48
 Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala
 1 5 10 15

aga ctt gcg att act gaa gaa gaa gca aaa atg ttc act gaa cag ctc 96
 Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu
 20 25 30

gac agt atc att tca ttt gcc gag gag ctt aat gag gtt aac aca gac 144
 Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp
 35 40 45

aat gtg gag cct aca act cac gtg ctg aaa atg aaa aat gtc atg aga 192
 Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg
 50 55 60

gaa gat gaa gcg ggt aaa ggt ctt ccg gtt gag gat gtc atg aaa aat 240
 Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn
 65 70 75 80

gcg cct gac cat aaa gac ggc tat att cgt gtg cca tca att ctg gac 288
 Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp
 85 90 95

taa 291

<210> 8

<211> 96

<212> PRT

<213> Bacillus subtilis

<400> 8

Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu Ala
 1 5 10 15

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Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln Leu
20 25 30

Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr Asp
35 40 45

Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met Arg
50 55 60

Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys Asn
65 70 75 80

Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu Asp
85 90 95